

AATAGATGCC GGGGCCCCAG AAGTCTTAGA CGTCGGGAAA GAGCAGCGCG AGAGCAGCGG GCGGCGCGCG CTGCGCTCTG GCGCAGCTTT TGGGACCCCA TTGAGGGAAT TtgaTCCAAG  
 GAGCTCTGA GATTGCGCGG GGAGAGAAAG CTCCTATATC ATTGTGTCCA CTTCAGGCG GGGAGGAGG AAGCGCGGA GCGGCGCTCT CGGCTGTCTC CGCAGCTGTC CACCTGCCCC  
 CATCTGCCG AGATCATGGT CTGCGGAGC CGAGCGGGA TGCTGTCTCT GCGGCGCGG CTACTGCGC TGCTGTCTCT CTGCTGTCTC CGGCTGCCG GAGCGCGGCG GCGCGCTCTG  
 35  
 M V C G S R G M L L L P A G L L A L A L C L L R V P G A R A A A C  
 GAGCCGCTTC GCATTTCCCT CTGCAAGTCC CTGCGCTGGA ACATGACTAA GATGCCCAAC CACCTGCACC ACAGCACCCA GGCACAGCC ATCCTGGCCA TCGAGCAGTT CGAAGCTCTG  
 75  
 E P V R I P L C K S L P W N M T K M P N H L H S T Q A N A I L A I E Q F E G L  
 CTGGCACCC ACTGCAGCCC GGATCTGCTC TTCTTCTCT GTGCTATGTA CGCGGCCATC TGCACCATTS ACTTCCAGCA CGAGCCCATC AAGCCCTGCA AGTCTGTGTG CGAGCGGCGC  
 115  
 L G T H C S P D L L F F L C A M Y A P I C T I D F Q H E P I K P C K S V C E R A  
 CGCAGGCGCT GTGAGGCCAT CCTCATCAAG TACGCCCACT CGTGGCCGGA AAGCCTGGCC TCGAGGAGC TGCCAGTATA TGACCGCGCG GTGTGCACT CTCCGAGGC CATCGTCACT  
 155  
 R Q G C E P I L I K Y R H S W P E S L A C E E L P V Y D R G V C I S P E A I V T  
 GCGCAGGAG CCGATTTTCC TATGATTC AGTAATGGAA ACTGTAGAGG AGCAGCAGT GAGCGTGA RATGTAAACC AGTCAGAGCT ACACAGAGA CCTATTTCG AACAATTAC  
 195  
 A D G A D F P M D S S N G N C R G A S S E R C K C K P V R A T Q K T Y F R N N Y  
 AACTATGCA TTCGGGCTAA AGTTAAGAA ATAAAGACCA AGTGTCTGTA TGTGACTGCA GTAGTGGAGG TGAAGAGAT TTAAAGGCT TCTCTGGTAA ACATTCACAG GGAACCTGTG  
 235  
 N Y V I R A K V K E I K T K C H D V T A V V E V K E I L K A S L V N I P R E I V  
 AACCTTTATA CCAGCTGCG CTGCGCTGTGT CTCACACTTA ACCTTAATGA GGATATCTC ATCATGGCT ACAGAGATGA AGAGCGCTCC AGATTACTGT TGGTAGAAGG TTCTATTGCT  
 275  
 N L Y T S S Q C L C P L N V N E E Y L I M E Y E D E E R S R L L L V E G S I A  
 GAGAAATGA AGGATCGACT TGGTAATAAA GTTAAGCGGT GGAATATGAA CGTCCGTCAT CTGGAGTGA ATACAAGTGA TTCTAGCCAT AGTGATTCCA CTCAGAGTCA GAAGCCTGGC  
 315  
 E K W K D R L G K K V K R W D M K L R H L G L N T S D S S H S D S T Q S Q K P G  
 AGGAATCTA ACTCCCGCA AGCAGCGCAC TAAATCCTGA AATGCAGAAA ATCTCAGT GACTTCTAT TAAGACTTGC ATTGCTGGAC TAGCAAGGC AATTCGACT ATTGCAGCTC  
 325  
 R N S N S R Q A R N  
 ATAGTCTATT TTTAGCCAC AAAATCAGG TGGTAATGA TATTACTTCT ATTTTCTCT TTGTTTCTG CTCTTCTCT TCCCGGATC CTTTTTGT GGTCTGAGTA CAGATCCTTA  
 AATATATAT ATGATTTCTA TTTCACATA CATGGGAAA CTGTTCTTTG CAATAATAT AATTAACA TGTGTATACC AGGCGCTCTT TGTGAGTA AATGTAAT TGTGTTCTG  
 CACCAGATT GGAATGCA TATTGGATC AAGAGAGAT TTCTGTGATA CAGAAAGC TAGTAGGT GTAAAGCATA CTGTCTCAT TTAATTACAG CCTATTCTT GCATGCTTT  
 TGGCATTCT CTCAGCTTA GAAATCTA AATGTTATA AAGGTAAAT GACAGTTTGA AATCAATGC CACAGGAG AGCAATCAG CACAGGAG CATTTATGAA GAATGACAC  
 ATGAGATGA TTAATTGCA GATTGGCAGG AAGCAAAATA AATGATTA GGAGCTGGG ATAGAGCATT TTGCTGACT GAGAAGCA ACTGAAGCTA GTAGCTGTG GGGTGTAAAC  
 AGCAGCAT TTCTTTGAC GATACATTG TTGTCTGTG AATATATGA TCAGCATTAG AGCAGTGGT TGTGACGCA CATCAGGTGT TATCAGATA GCTCTGTTA ATTGCTTCC  
 TTTAGATGA ACGCATTG GTCTTTTT TCTTCTTTA AATTAATCT CCCTTGTGTC AATATATGA CATATATGA TGTGACCGG GCTGTATT TTAAGATATG  
 TAGCTCTATA AACGCTATA GTCAAAGAT GGTAAATGT GCAAGATTCT GGGTGTGTG ATTAATGTGT GTGTGCTCGC ATACACTC ACTCAAGCTG AACTGAACGA CAGGCTGTG  
 CACTGCGCTG CACTTATCA TTTGGAATTG TGCTGTGTTAA TGTCTAGTAA AATATGCTTA ATAAAGAA AAAAAAAA AAAAAAAA AAAA

FIG. 1

bovine	MVCGSR	<u>SGML LLPAGLLALAL ALCLLR</u>	PGA	RAACEPVRI	PLCKSLPWNM	50
human	-----P-----	-----R-----	-----	-----	-----	50
bovine	TKMPNHLHHS	TQANAILAIE	<u>QFEGLLGTHC</u>	<u>SPDLLFFLCA</u>	<u>MYAPICTIDF</u>	100
human	-----	-----	-----	-----	-----	100
bovine	QHEPIKPKCS	VCERARQGCE	PILIKYRHSW	PESLACEELP	VYDRGVCISP	150
human	-----	-----	-----	--N-----	-----	150
bovine	EAIVTADGAD	FPMDSSNGNC	RGASSERCKC	KPVRATQKTY	FRNNYNYVIR	200
human	-----	-----	-----	--I-----	-----	200
bovine	AKVKEIKTKC	HDVTAVVEVK	EILKASLVNI	PRETVNLYTS	SGCLCPPLNV	250
human	-----	-----	---S-----	--D-----	-----	250
bovine	NEEYLIMGYE	DEERSRLLLV	EGSIAEKWKD	RLGKKVKRWD	MKLRHLGLNT	300
human	---I-----	-----	-----	-----	-----SK	300
bovine	SDSSHSDSTQ	SQKPGRNSNS	RQARN			325
human	---N-----	---S-----	---P-----	-----	-----	325

FIG. 2A

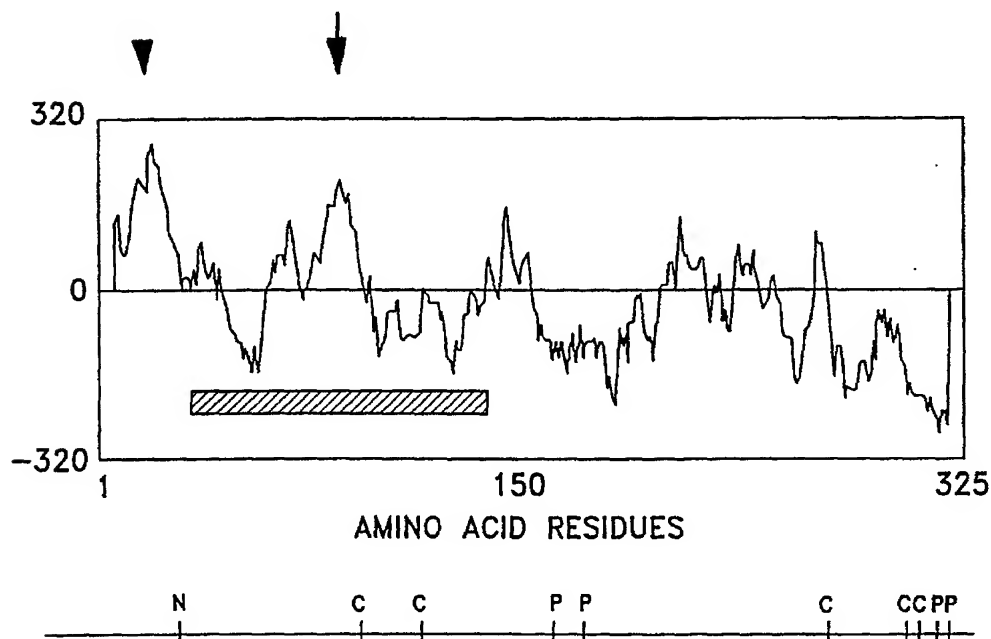


FIG. 2B

Rat fz-1	QEPISLDELDT	DIAYNQHMMP	NLIGCHNQED	AGLEVHQFYP	IVKVQCSAEI	160
Drosophila frizzled	CEPITISICK	NIPYNNMMP	NLIGCHNQEE	AGLEVHQEAP	IVKIGCSDIL	102
bovine frzb	CEPVRRIPLCK	SLEFNNMMP	NHLEHSTQAN	ATLAIEQFEG	ILGTHCSPDL	84
human frzb	CEPVRRIPLCK	SLEFNNMMP	NHLEHSTQAN	ATLAIEQFEG	ILGTHCSPDL	84
	*			*		
Rat fz-1	KQFLCSVMAP	VCTVLEQALP	--PQRSICER	AR--CCCHALMN	KQGFQWPDIL	207
Drosophila frizzled	QIFLCSVMMP	VCTVLERPIP	--PQRSICES	AR-VCEKLMK	TNNFNWPENL	149
bovine frzb	LEFLQVMAP	ICTIDFQHEP	IKPKSVCHER	ARQCCRPILI	KMRHSWPESL	134
human frzb	LEFLQVMAP	ICTIDFQHEP	IKPKSVCHER	ARQCCRPILI	KMRHSWPENL	134
	*	*	*	*		
Rat fz-1	KCEKFPVHCG	GEIC				221
Drosophila frizzled	EQSKFPVHGG	EDIC				163
bovine frzb	ACEEILPVYDR	G-VC				147
human frzb	ACEEILPVYDR	G-VC				147
	*	*				

FIG.3

xFrzb	MSPTKLDSE	II----	LIVIP	GIWLLILNA	YCSCEPVRI	PCKSLPMNM	46
bFrzb	MVCSRGGL	LLPAGLLALA	ALJLIRVEGA	RAAAACEPVRI	PLCKSLPMNM		50
hFrzb	MVCSPPGML	ILRAGLLALA	ALJLIRVEGA	RAAAACEPVRI	PLCKSLPMNM		50
Consensus	MVCS.GGML	IL.L.AGLIALA	ALJLIRVEGA	RAAAACEPVRI	PLCKSLPMNM		50
xFrzb	TKMPNHLHHS	TOANAIIAIE	QFEGLIJHEC	SPDLLFFFLCA	MYAPICTIDE		96
bFrzb	TKMPNHLHHS	TOANAIIAIE	QFEGLIJHEC	SPDLLFFFLCA	MYAPICTIDE		100
hFrzb	TKMPNHLHHS	TOANAIIAIE	QFEGLIJHEC	SPDLLFFFLCA	MYAPICTIDE		100
Consensus	TKMPNHLHHS	TOANAIIAIE	QFEGLIJHEC	SPDLLFFFLCA	MYAPICTIDE		100
xFrzb	QHEPIKPCKS	VCEARAGCE	PILIKYRHSW	PESLACEELP	VDRGVGCISP		146
bFrzb	QHEPIKPCKS	VCEARAGCE	PILIKYRHSW	PESLACEELP	VDRGVGCISP		150
hFrzb	QHEPIKPCKS	VCEARAGCE	PILIKYRHSW	PENLACEELP	VDRGVGCISP		150
Consensus	QHEPIKPCKS	VCEARAGCE	PILIKYRHSW	PESLACEELP	VDRGVGCISP		150
xFrzb	AEIVTAD-G	DSMHDFPMD	NNGNQSSG	STAG	ERCKCKPMRA	SQKTYLKNNY	196
bFrzb	EAIVTAD-G	---ADFPMDS	SNGNORGASS		ERCKCKPVRA	IKQTYFRNNY	195
hFrzb	EAIVTAD-G	---ADFPMDS	SNGNORGASS		ERCKCKPTRA	IKQTYFRNNY	195
Consensus	EAIVTAD-G	---ADFPMDS	SNGNORGASS		ERCKCKH.RA	IKQTYFRNNY	200
xFrzb	NYVIRAKVKE	VAKICHIVTA	IWEVKEILKS		SLVNTHKDTV	ILVNTSSGCLC	246
bFrzb	NYVIRAKVKE	IKIKCHIVTA	WEVKEILNA		SLVNTHRETV	NLYTSSGCLC	245
hFrzb	NYVIRAKVKE	IKIKCHIVTA	WEVKEILKS		SLVNTHRDIV	NLYTSSGCLC	245
Consensus	NYVIRAKVKE	IKIKCHIVTA	WEVKEILKS		SLVNTHRDIV	NLYTSSGCLC	250
xFrzb	PPINVNEEYI	IMGYEDEERS			RULLIVEGSLA	EKKWDRIGKK	296
bFrzb	PPINVNEEYI	IMGYEDEERS			RULLIVEGSLA	EKKWDRIGKK	295
hFrzb	PPINVNEEYI	IMGYEDEERS			RULLIVEGSLA	EKKWDRIGKK	295
Consensus	PPINVNEEYI	IMGYEDEERS			RULLIVEGSLA	EKKWDRIGKK	300
xFrzb	-----PRK	SKDPVAPIPN	KNSNSROARS				319
bFrzb	LGLNTSDSSH	SDSTQSQKPG	RNSNSROARN				325
hFrzb	LGLSKSDSSN	SKSTQSQKSG	RNSNSROARN				325
Consensus	LGL..SDSS.	SDSTQSQKPG	RNSNSROARN				330

FIG. 4

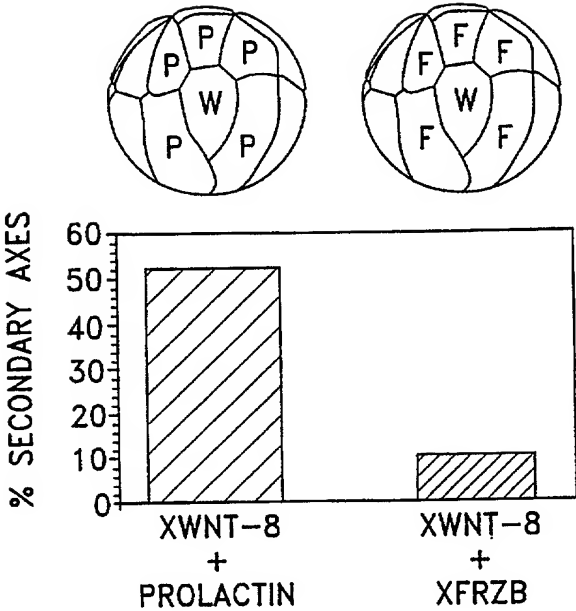


FIG.5

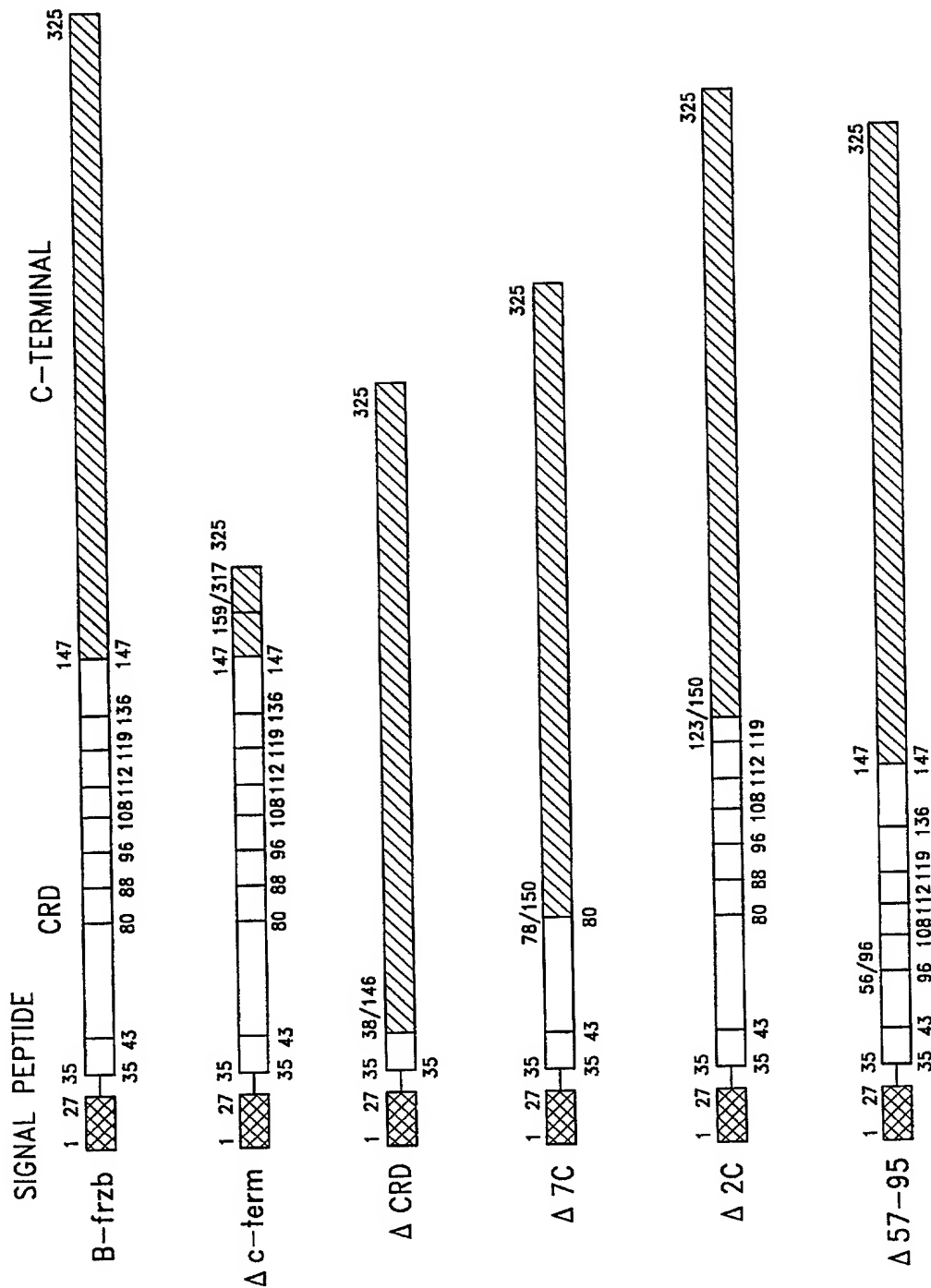
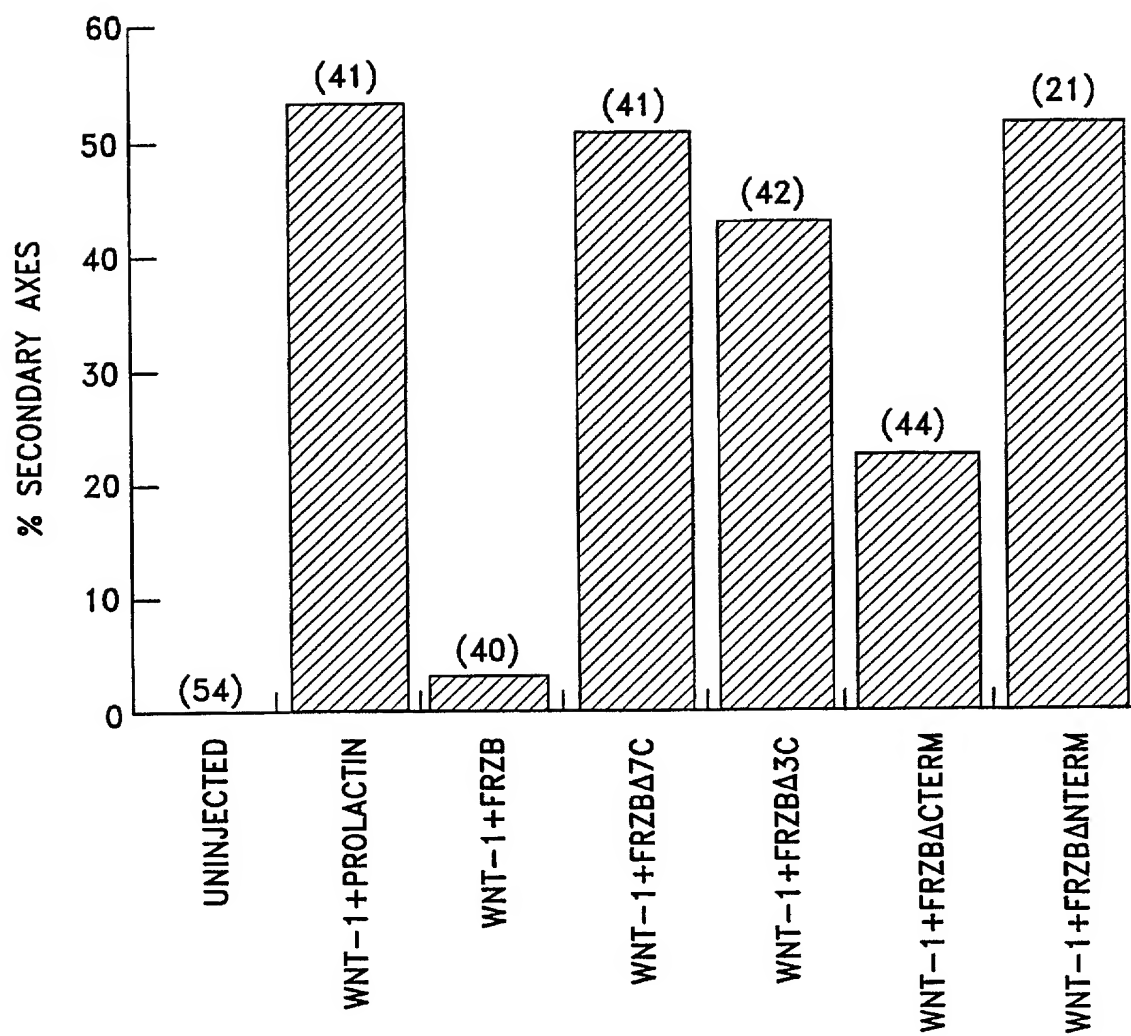


FIG.6

*FIG. 7*